OIPE

DATE: 12/07/2001 RAW SEQUENCE LISTING TIME: 12:18:52 PATENT APPLICATION: US/09/961,201

Input Set : N:\Crf3\RULE60\09961201.txt

Output Set: N:\CRF3\12072001\I961201.raw

SEQUENCE LISTING

```
3 (1) GENERAL INFORMATION:
             (i) APPLICANT: DIXIT, VISHVA M.
     5
                            HE, WEI-WU
     6
                            KIKLY, KRISTINE K.
     7
                            RUBEN, STEVEN M.
     8
            (ii) TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
    10
                                     ENZYME LIKE APOPTOTIC PROTEASE-6
    11
           (iii) NUMBER OF SEQUENCES: 11
    13
            (iv) CORRESPONDENCE ADDRESS:
     15
                  (A) ADDRESSEE: Ratner & Prestia
     16
                  (B) STREET: P.O. Box 980
     17
                  (C) CITY: Valley Forge
     18
                  (D) STATE: PA
     19
                  (E) COUNTRY: USA
                                                             ENTED
     20
     21
                  (F) ZIP: 19482
             (V) COMPUTER READABLE FORM:
     23
                  (A) MEDIUM TYPE: Diskette
     24
                  (B) COMPUTER: IBM Compatible
     25
                  (C) OPERATING SYSTEM: DOS
     26
                  (D) SOFTWARE: FastSEQ for Windows Version 2.0
     27
            (vi) CURRENT APPLICATION DATA:
     29
                  (A) APPLICATION NUMBER: US/09/961,201
C--> 30
                  (B) FILING DATE: 24-Sep-2001
C--> 31
                  (C) CLASSIFICATION:
     32
           (vii) PRIOR APPLICATION DATA:
     34
                  (A) APPLICATION NUMBER: 09/300,328
     36
                  (B) FILING DATE:
     37
                  (A) APPLICATION NUMBER: US/08/852,936
     39
                  (B) FILING DATE: 08-MAY-1997
     40
                  (A) APPLICATION NUMBER: 60/018,961
     42
                  (B) FILING DATE: 05-JUN-1996
     43
                  (A) APPLICATION NUMBER: 60/020,344
     45
                  (B) FILING DATE: 23-MAY-1996
     46
                  (A) APPLICATION NUMBER: 60/017,949
     48
                  (B) FILING DATE: 20-MAY-1996
     49
          (viii) ATTORNEY/AGENT INFORMATION:
     51
                  (A) NAME: Prestia, Paul F
     52
                  (B) REGISTRATION NUMBER: 23,031
     53
                   (C) REFERENCE/DOCKET NUMBER: p50483-2
     54
            (ix) TELECOMMUNICATION INFORMATION:
     56
                   (A) TELEPHONE: 610-407-0700
     57
                   (B) TELEFAX: 610-407-0700
     58
                   (C) TELEX: 846169
     59
     62 (2) INFORMATION FOR SEQ ID NO: 1:
             (i) SEQUENCE CHARACTERISTICS:
     64
```

65

(A) LENGTH: 416 amino acids

RAW SEQUENCE LISTING DATE: 12/07/2001 PATENT APPLICATION: US/09/961,201 TIME: 12:18:52

Input Set : N:\Crf3\RULE60\09961201.txt
Output Set: N:\CRF3\12072001\1961201.raw

67 (C) STRANDEDNESS: single 68 (D) TOPOLOGY: linear 70 (ii) MOLECULE TYPE: protein 72 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: 74 Met Asp Glu Ala Asp Arg Arg Leu Leu Arg Arg Cys Arg Leu Arg Leu 75 1 5 10 15 76 Val Glu Glu Leu Glu Val Asp Gln Leu Trp Asp Val Leu Leu Ser Arg 77 20 25 30 78 Glu Leu Phe Arg Pro His Met Ile Glu Asp Ile Gln Arg Ala Gly Ser 78 35 40 45 80 Gly Ser Arg Arg Asp Gln Ala Arg Gln Leu Ile Ile Asp Leu Glu Thr 81 50 55 60 81 61 Ser Gln Ala Leu Pro Leu Phe Ile Ser Cys Leu Glu Asp Thr 82 62 Arg Gly Ser Gln Ala Leu Pro Leu Phe Ile Ser Cys Leu Glu Asp Thr 83 65 70 85 86 Gly Gln Asp Met Leu Ala Ser Phe Leu Arg Thr Asn Arg Gln Ala Gly 87 90 88 61 Lys Leu Ser Lys Pro Thr Leu Glu Asn Leu Thr Pro Val Val Leu Arg 87 100 88 Pro Glu Ile Arg Lys Pro Glu Val Leu Arg Pro Glu Thr Pro Arg Pro 89 115 120 120 121 120 121 130 92 Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys 134 Asp Ile Gly Ser Gly Gly Phe Gly Asp Val Gly Ala Leu Glu Ser 91 130 135 92 Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys 145 150 155 160 94 Gly His Cys Leu Ile Ile Asn Asn Asn Val Asn Phe Cys Arg Glu Ser Gly 160 165 170 175 95 Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg 97 180 185 98 Arg Phe Ser Ser Leu His Phe Met Val Glu Leu Ala Arg Gln Asp His 101 210 225 102 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys 104 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys 105 225 106 Pro Val Ser Val Glu Lys Ile Val Asn Ile Leu Ser His Gly Cys Glu 107 260 265 108 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Arg Gln Asp His 109 275 110 Gly Glu Gln Lys Asp His Gly Phe Glu Val Asa Fr Thr Ser Pro Glu 111 290 295 112 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Glu 113 305 310 305 1310 1325 1340 1340 1351 1361 1375 1376 1376 1377 1387 1387 1388 1389 1380 1380 1380 1380 1380 1380 1380 1380	66 (B) TYPE: amino acid																
(ii) Molecule Type: protein	67 (C) STRANDEDNESS: single																
Table Sequence Description: SEQ ID No: 1: Table Sequence																	
74 Met Asp Glu Ala Asp Arg Arg Leu Leu Arg Arg Cys Arg Leu Arg Leu 1 1 15 15 15 15 15 15 15 15 15 15 16 Val Glu Glu Leu Gln Val Asp Gln Leu Trp Asp Val Leu Leu Ser Arg 16 Val Glu Leu Phe Arg Pro His Met Ile Glu Asp Ile Gln Arg Ala Gly Ser Arg 20 25 30 30 31	70		(ii)	MOLI	ECULE	TYP	E: p	rote	ein			_					
To To To To To To To To	72		(xi)	SEQU	JENCE	DES	SCRIF	MOIT	I: SE	EQ II	ONO:	: 1:	_	_	.	3	т
1	74	Met	Asp	Glu	Ala		Arg	Arg	Leu	Leu		Arg	Cys	Arg	Leu	Arg	Leu
The column The	75	1								_		_	**- 1	.	т		7 200
Glu Leu Phe Arg Pro His Met Ile Glu Asp Ile Gln Arg Ala Gly Ser 79	76	Val	Glu	Glu	Leu	Gln	Val	Asp	Gln	Leu	Trp	Asp	Val	ьeu	Leu	ser	Arg
679 35 40 45 800 Gly Ser Arg Arg Arg Asp Gln Ala Arg Gln Leu II e II e Asp Leu Glu Thr 50 55 60 82 Arg Gly Ser Gln Ala Leu Pro Leu Phe II e Ser Cys Leu Glu Asp 75 80 84 Gly Gln Asp Met Leu Ala Ser Phe Leu Arg Thr Asn Arg Gln Ala Gly 80 85 85 90 95 86 Lys Leu Ser Lys Pro Thr Leu Glu Asn Leu Thr Pro Val Val Leu Arg 110 87 100 105 110 88 Pro Glu II e Arg Lys Pro Glu Val Leu Arg Pro Glu Thr Pro Arg Pro 110 89 115 120 125 90 Val Asp II e Gly Ser Gly Gly Phe Gly Asp Val Gly Ala Leu Glu Ser 110 91 130 135 140 92 Leu Arg Gly Asn Ala Asp Leu Ala Tyr II e Leu Ser Met Glu Pro Cys 160 94 Gly His Cys Leu II e II e Asn Asn Val Asn Phe Cys Arg Glu Ser Gly 95 165 170 175 96 Leu Arg Thr Arg Thr Gly Ser Asn II e Asp Cys Glu Lys Leu Arg Arg 190 97 180 185 190	77				20									_		a1	0.00
Gly Ser Arg Arg Asp Gln Ala Arg Gln Leu Ile Ile Asp Leu Glu Thr 55 60 22 Arg Gly Ser Gln Ala Leu Pro Leu Phe Ile Ser Cys Leu Glu Asp Thr 36 65 70 75 80 84 Gly Gln Asp Met Leu Ala Ser Phe Leu Arg Thr Asn Arg Gln Ala Gly 85 90 95 86 Lys Leu Ser Lys Pro Thr Leu Glu Asn Leu Thr Pro Val Val Leu Arg 87 100 105 110 88 Pro Glu Ile Arg Lys Pro Glu Val Leu Arg Pro Glu Thr Pro Arg Pro 115 120 125 90 Val Asp Ile Gly Ser Gly Gly Phe Gly Asp Val Gly Ala Leu Glu Ser 1130 135 140 92 Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys 145 150 160 94 Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly 95 145 150 155 160 94 Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr 97 180 185 190 98 Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr 195 200 205 100 Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His 101 210 215 220 102 Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln 225 230 235 240 104 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys 105 260 275 106 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys 107 260 265 270 108 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly 109 275 280 285 110 Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu 112 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Glu 113 305 310 315 320 114 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Thr Pro Phe Gln 115 325 330 335 116 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val	78	Glu	Leu	Phe	Arg	Pro	His	Met		GLu	Asp	TTE	GIN	Arg	Ата	GIY	ser
81	79			35			_			~ 3	_	~1 -	-1 -	_	T 011	Clu	mh.c
Arg Gly Ser Gln Ala Leu Pro Leu Phe Ile Ser Cys Leu Glu Asp Thr 83 65 70 75 80 84 Gly Gln Asp Met Leu Ala Ser Phe Leu Arg Thr Asn Arg Gln Ala Gly 85 90 95 85 90 95 86 Lys Leu Ser Lys Pro Thr Leu Glu Asn Leu Thr Pro Val Val Leu Arg 110 105 110 88 Pro Glu Ile Arg Lys Pro Glu Val Leu Arg Pro Glu Thr Pro Arg Pro 120 125 90 Val Asp Ile Gly Ser Gly Gly Phe Gly Asp Val Gly Ala Leu Glu Ser 130 135 140 91 Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Ser Gly Gly Phe Gly Ala Nan Phe Cys Arg Glu Ser Gly Gly Phe Gly Ala Pro 155 160 94 Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly Gly Phe Met Val Glu Val Lys Leu Arg Arg Arg 160 98 Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Leu Arg Arg Arg 190 98 Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr 190 98 Arg Phe Ser Ser Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His 210 210 215 220 100 Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His 210 221 220 102 Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys 104 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys 255 106 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys 265 107 260 108 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly 295 109 275 280 110 305 310 315 120 325 450 325 450 326 461 327 482 328 483 484 484 485 484 485 484 485 485 485 485	80	Gly	Ser	Arg	Arg	Asp	Gln		Arg	GIn	Leu	TTE	TTE	ASP	Leu	GIU	TIIT
83 65	81		50			_			_		- 1-	a		T 011	Clu	7 cn	Thr
63		_	Gly	Ser	Gln	Ala		Pro	Leu	Pne	ше	5er	Cys	цец	GLU	кар	80
S		65	_			_	70	~	D1	T	7		7 an	λνα	Cln	λla	
86		Gly	Gln	Asp	Met		Ala	ser	Pne	ьeu		THE	ASII	AIG	GIII	95	GLY
100					_	85		.	01	3		mh r	Dro	Val	Va 1		Δra
88		Lys	Leu	Ser		Pro	Thr	Leu	GIU	ASI	Leu	1111	PIO	Val	110	пси	1119
115					100		D	a1	37 n 1		7 mar	Dro	Glu	Thr		Δrσ	Pro
89 Val Asp Ile Gly Ser Gly Gly Phe Gly Asp Val Gly Ala Leu Glu Ser 91 130 135 140 92 Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys 93 145 150 155 160 94 Gly His Cys Leu Ile Ile Asn Asn Syn Val Asn Phe Cys Arg Glu Ser Gly 165 170 175 96 Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg 185 190 98 Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr 190 90 195 200 205 100 Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His 215 101 210 215 220 102 Gly Ala Leu Asp Cys Cys Val Val Val Val Leu Ala Arg Gln Asp His 215 103 225 230 235 240 104 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys Gln 225 105 245 250 250 255 106 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys 270 108 Pro Ser Leu Gly Gly Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu 10 27		Pro	Glu		Arg	Lys	Pro	GIU		ьeu	Arg	PIO	GIU	125	FIU	nrg	110
130			_	115	a 3.	0	01	a1		C1.	7 cn	V = 1	Glv		T.e.11	Glu	Ser
Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys 145 150 155 160 94 Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly 165 170 175 96 Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg 180 185 190 98 Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr 99 195 200 205 100 Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His 101 210 215 220 102 Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln 103 225 230 235 104 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys 105 245 250 260 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys 107 260 265 270 108 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly 109 275 280 285 110 Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu 111 290 295 300 112 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln 13 305 310 335 16 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val		Val			GLY	ser	GIY		Pne	СТУ	ASP	Val	1/10	ALU	шси	O L u	001
93 145		_	130	a1	3	3. 1. 0	A an		λla	Trans	ΤlΔ	T.011		Met	Glu	Pro	Cvs
94 Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly 95				GIY	ASII	Ald		пеп	ΑΙα	тут	11.0	155	DCI	1100	0		160
95 Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg 97 180 185 190 98 Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr 99 195 200 205 100 Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His 101 210 215 220 102 Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln 103 225 230 235 240 104 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys 105 245 255 106 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys 107 260 265 270 108 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly 109 275 280 110 Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu 111 290 295 300 112 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln 113 305 310 315 320 114 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro 115 325 Tyr Ser Thr Phe Pro Gly Phe Val		145	TT d on	Crra	T OIL	T10	T10	λen	Δen	Val	Asn		Cvs	Ara	Glu	Ser	Gly
See Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg 180 185 190 190 190 195 200 205 180 205 180 180 180 180 180 180 180 190 190 195 200 205 180		GIY	HIS	Cys	ьеи		116	NSII	ASII	val	170	1 110	012	5		175	-
98 Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr 99 195 200 205 100 Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His 101 210 215 220 102 Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln 103 225 230 235 240 104 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys 105 245 255 106 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys 107 260 265 270 108 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly 109 275 280 285 110 Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu 111 290 295 300 112 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln 113 305 310 315 320 114 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro 115 325 335 116 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val		T 011	7 ~ ~	Thr	λνα		Glv	Ser	Asn	Tle			Glu	Lvs	Leu	Arg	Arg
98 Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr 99 195 200 205 100 Ala Lys Lys Met Val Leu Ala Leu Glu Leu Ala Arg Gln Asp His 210 215 220 102 Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln 235 240 103 225 230 235 240 104 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys 240 105 245 250 255 106 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys 260 265 107 260 265 270 108 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly 285 110 Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu 285 110 Gly Glu Gln Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln 320 112 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln 320 114 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro 330 335 116 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pr		ьеи	AIG	TIIT		1111	OLY	501	11011			-1-		-	190	•	_
99		λνα	Dhe	Ser	Ser	Len	His	Phe	Met			Val	Lys	Gly	Asp	Leu	Thr
100		тту	riic			Dou							-	205			
101		1Δ (a Lv	s Lv	s Mei	t. Va	1 Le	ı Ala		u Le	u Gl	u Le	u Al	a Ar	g Gl	n Asj	p His
102 Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln 103 225		l	21	0				21	5				22	0			
103 225 230 235 240		2 G1	v Al	a Le	u Ası	р Су	s Cy	s Va	l Va	l Va	1 I1	e Le	u Se	r Hi	s Gl	у Су	s Gln
104 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys 105 106 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys 107 108 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly 109 275 110 Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu 111 290 295 112 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln 113 305 114 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro 115 116 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val		3 22	5				23	0				23	5				240
105 106 107 108 109 109 109 110 110 111 110 1290 1112 111 111 111 111 111 111 111 111 1		ı Al	a Se	er Hi	s Le	u Gl	n Ph	e Pr	o Gl	y Al	a Va	l Ty	r Gl	y Th	r As	p Gl	y Cys
106 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys 107 260 265 270 108 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly 109 275 280 285 110 Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu 111 290 300 112 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln 113 305 310 114 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro 115 325 116 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val		5				24	5				25	0				25	5
107		5 Pr	o Va	ıl Se	r Va	1 Gl	u Ly	s Il	e Va	l As	n Il	e Ph	e As	n Gl	y Th	r Se	r Cys
108 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly 109		7			26	0				26	5				27	0	
109		3 Pr	o Se	er Le	u Gl	y Gl	у Lу	s Pr	о Гу	s Le	u Ph	e Ph	e Il	e Gl	n Al	a Cy	s Gly
111 290 295 300 112 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln 113 305 310 315 320 114 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro 115 325 330 335 116 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val		a		2.7	5				28	0				28	כ		
111 290 295 300 112 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln 113 305 310 315 320 114 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro 115 325 330 335 116 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val	11) G1	y G]	u Gl	n Ly	s As	p Hi	s Gl	y Ph	e Gl	u Va	l Al	a Se	r Th	r Se	r Pr	o GIu
113 305 310 315 320 114 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro 115 325 330 335 116 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val	11	1	29	0				29	5				30	0			
113 305 310 315 320 114 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro 115 325 330 335 116 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val	11	2 As	p G]	u Se	r Pr	o Gl	y Se	r As	n Pr	o Gl	u Pr	o As	p Al	a Th	r Pr	o Ph	e GIn
115 325 330 335 116 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val		3 30	5				31	0				31	5				320
116 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val	11	4 Gl	.u G]	y Le	u Ar			e As	p Gl	n Le	u As	p Al	a Il	e Se	r Se	r Le	u Pro
- · - 250	11	5				32	5		_						_ 01		
117 340 345 350	11	6 Th	ır Pı	o Se			e Ph	e Va	ı Se	r Ty	r Se	r Th	r Ph	e Pr	O GI	v A bu	e vai
	11	7			34	0				34	5				33	U	

RAW SEQUENCE LISTING

DATE: 12/07/2001

PATENT APPLICATION: US/09/961,201

TIME: 12:18:53

Input Set : N:\Crf3\RULE60\09961201.txt
Output Set: N:\CRF3\12072001\I961201.raw

```
Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
118
                                 360
                                                      365
             355
119
     Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu
120
                             375
                                                  380
121
    Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
122
                         390
                                              395
123
     Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
124
                                         410
                     405
125
    (2) INFORMATION FOR SEQ ID NO: 2:
127
         (i) SEQUENCE CHARACTERISTICS:
129
              (A) LENGTH: 1578 base pairs
130
              (B) TYPE: nucleic acid
131
              (C) STRANDEDNESS: single
132
              (D) TOPOLOGY: linear
133
        (ii) MOLECULE TYPE: cDNA
135
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
137
                                                                           60
139 GCCATGGACG AAGCGGATCG GCGGCTCCTG CGGCGGTGCC GGCTGCGGCT GGTGGAAGAG
140 CTGCAGGTGG ACCAGCTCTG GGACGTCCTG CTGAGCCGCG AGCTGTTCAG GCCCCATATG
                                                                          120
141 ATCGAGGACA TCCAGCGGGC AGGCTCTGGA TCTCGGCGGG ATCAGGCCAG GCAGCTGATC
                                                                          180
142 ATAGATCTGG AGACTCGAGG GAGTCAGGCT CTTCCTTTGT TCATCTCCTG CTTAGAGGAC
                                                                          240
                                                                          300
143 ACAGGCCAGG ACATGCTGGC TTCGTTTCTG CGAACTAACA GGCAAGCAGG AAAGTTGTCG
144 AAGCCAACCC TAGAAAACCT TACCCCAGTG GTGCTCAGAC CAGAGATTCG CAAACCAGAG
                                                                          360
145 GTTCTCAGAC CGGAAACACC CAGACCAGTG GACATTGGTT CTGGAGGATT CGGTGATGTC
                                                                          420
146 GGTGCTCTTG AGAGTTTGAG GGGAAATGCA GATTTGGCTT ACATCCTGAG CATGGAGCCC
147 TGTGGCCACT GCCTCATTAT CAACAATGTG AACTTCTGCC GTGAGTCCGG GCTCCGCACC
                                                                          540
148 CGCACTGGCT CCAACATCGA CTGTGAGAAG TTGCGGCGTC GCTTCTCCTC GCTGCATTTC
                                                                          600
149 ATGGTGGAGG TGAAGGGCGA CCTGACTGCC AAGAAAATGG TGCTGGCTTT GCTGGAGCTG
                                                                          660
150 GCGCGGCAGG ACCACGGTGC TCTGGACTGC TGCGTGGTGG TCATTCTCTC TCACGGCTGT
                                                                          720
151 CAGGCCAGCC ACCTGCAGTT CCCAGGGGCT GTCTACGGCA CAGATGGATG CCCTGTGTCG
                                                                          780
152 GTCGAGAAGA TTGTGAACAT CTTCAATGGG ACCAGCTGCC CCAGCCTGGG AGGGAAGCCC
                                                                          840
153 AAGCTCTTTT TCATCCAGGC CTGTGGTGGG GAGCAGAAAG ACCATGGGTT TGAGGTGGCC
                                                                          900
154 TCCACTTCCC CTGAAGACGA GTCCCCTGGC AGTAACCCCG AGCCAGATGC CACCCCGTTC
155 CAGGAAGGTT TGAGGACCTT CGACCAGCTG GACGCCATAT CTAGTTTGCC CACACCCAGT
                                                                         1020
156 GACATCTTTG TGTCCTACTC TACTTTCCCA GGTTTTGTTT CCTGGAGGGA CCCCAAGAGT
                                                                         1080
157 GGCTCCTGGT ACGTTGAGAC CCTGGACGAC ATCTTTGAGC AGTGGGCTCA CTCTGAAGAC
                                                                         1140
158 CTGCAGTCCC TCCTGCTTAG GGTCGCTAAT GCTGTTTCGG TGAAAGGGAT TTATAAACAG
                                                                         1200
159 ATGCCTGGTT GCTTTAATTT CCTCCGGAAA AAACTTTTCT TTAAAACATC ATAAGGCCAG
                                                                         1260
160 GGCCCCTCAC CCTGCCTTAT CTTGCACCCC AAAGCTTTCC TGCCCCAGGC CTGAAAGAGG
                                                                         1320
161 CTGAGGCCTG GACTTTCCTG CAACTCAAGG ACTTTGNAGC CGGCACAGGG TCTGCTCTTT
                                                                         1380
162 CTCTGCCAGT GACAGACAGG CTCTTAGCAG CTTCCAGATT GACGACAAGT GCTGAACAGT
163 GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGTGG NCTCTTGAGC AGTGGCTGGT
                                                                         1500
164 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTAGGAG CAGGGATTAA
                                                                         1560
                                                                         1578
165 CCTCTGCACT ACTGACAT
167 (2) INFORMATION FOR SEQ ID NO: 3:
         (i) SEQUENCE CHARACTERISTICS:
169
              (A) LENGTH: 639 base pairs
170
              (B) TYPE: nucleic acid
171
              (C) STRANDEDNESS: single
172
              (D) TOPOLOGY: linear
173
```

60

DATE: 12/07/2001 RAW SEQUENCE LISTING PATENT APPLICATION: US/09/961,201 TIME: 12:18:53

Input Set : N:\Crf3\RULE60\09961201.txt Output Set: N:\CRF3\12072001\I961201.raw

```
(ii) MOLECULE TYPE: cDNA
175
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
177
179 CTGACTGCCA AGAAAATGGT GCTGGCTTTG CTGGAGCTGG CGCGGCAGGA CCACGGTGCT
180 CTGGACTGCT GCGTGGTGGT CATTCTCTCT CACGGCTGTC AGGCCAGCCA CCTGCAGTTC
                                                                          120
181 CCAGGGGCTG TCTACGGCAC AGATGGATGC CCTGTGTCGG TCGAAAAGAT TGTGAACATC
                                                                          180
182 TTCAATGGGA CCAGCTGCCC CAGCCTGGGA GGGAAGCCCA AGCTCTTTTT CATCCAGGCC
183 TGTGGTGGGG AGCAGAAGA CCATGGGTTT GAGGTGGCCT CCACTTCCCC TGAAGACGAG
184 TCCCCTGGCA GTAACCCCGA GCCAGATGCC ACCCCGTTCC AGGAAGGTTT GAGGACCTTC
185 GACCAGCTGG ACGCCATATC TAGTTTGCCC ACACCCAGTG ACATCTTTGT GTCCTACTCT
                                                                          420
186 ACTTTCCCAG GTTTTGTTTC CTGGAGGGAC CCCAAGAGTG GCTCCTGGTA CGTTGAGACC
187 CTGGACGACA TCTTTGAGCA GTGGGCTCAC TCTGAAGACC TGCAGTCCCT CCTGCTTAGG
                                                                          540
188 GTCGCTAATG CTGTTTCGGT GAAAGGGATT TATAAACAGA TGCCTGGTTG CTTTAATTTC
                                                                          600
189 CTCCGGAAAA AACTTTTCTT TTAAAACATC ATAAGGCAG
                                                                          639
191 (2) INFORMATION FOR SEQ ID NO: 4:
193
         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 203 amino acids
194
195
              (B) TYPE: amino acid
196
              (C) STRANDEDNESS: single
197
              (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: protein
199
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
201
     Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His Gly Ala Leu
203
204
                                          10
205
     Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln Ala Ser His
206
                                      25
                 20
     Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys Pro Val Ser
207
208
                                 40
209
     Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys Pro Ser Leu
                             55
210
     Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly Gly Glu Gln
211
                         70
                                              75
212
     Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu Asp Glu Ser
213
214
                                          90
215
     Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln Glu Gly Leu
                                      105
                                                          110
216
                 100
217
     Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro Thr Pro Ser
                                 120
218
     Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val Ser Trp Arg
219
                                                  140
220
                             135
221
     Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp Asp Ile Phe
222
                         150
                                              155
     Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu Leu Arg Val
223
                                                              175
224
                     165
                                          170
     Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met Pro Gly Cys
225
226
     Phe Asn Phe Leu Arg Lys Leu Phe Phe Met
227
228
             195
                                 200
230 (2) INFORMATION FOR SEQ ID NO: 5:
         (i) SEQUENCE CHARACTERISTICS:
```



DATE: 12/07/2001 TIME: 12:18:53

PATENT APPLICATION: US/09/961,201

Input Set : N:\Crf3\RULE60\09961201.txt
Output Set: N:\CRF3\12072001\1961201.raw

```
233
               (A) LENGTH: 34 base pairs
234
               (B) TYPE: nucleic acid
235
               (C) STRANDEDNESS: single
236
               (D) TOPOLOGY: linear
238
         (ii) MOLECULE TYPE: cDNA
240
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
242 GAACGGGTA CCGCCATGGA CGAAGCGGAT CGGC
                                                                           34
244 (2) INFORMATION FOR SEQ ID NO: 6:
246
         (i) SEQUENCE CHARACTERISTICS:
247
               (A) LENGTH: 60 base pairs
248
               (B) TYPE: nucleic acid
249
               (C) STRANDEDNESS: single
250
               (D) TOPOLOGY: linear
252
        (ii) MOLECULE TYPE: cDNA
254
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
256 TGCTCTAGAT TAGTGGTGGT GGTGGTGGTG TGATGTTTTA AAGAAAAGTT TTTTCCGGAG
                                                                            60
258 (2) INFORMATION FOR SEQ ID NO: 7:
260
         (i) SEQUENCE CHARACTERISTICS:
261
              (A) LENGTH: 41 base pairs
262
              (B) TYPE: nucleic acid
263
              (C) STRANDEDNESS: single
264
              (D) TOPOLOGY: linear
266
        (ii) MOLECULE TYPE: cDNA
268
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
270 AAGCTCTTTT TCATCCAGGC CGCGGGTGGG GAGCAGAAGA C
                                                                            41
272 (2) INFORMATION FOR SEQ ID NO: 8:
274
        (i) SEQUENCE CHARACTERISTICS:
275
              (A) LENGTH: 39 base pairs
276
              (B) TYPE: nucleic acid
277
              (C) STRANDEDNESS: single
278
              (D) TOPOLOGY: linear
280
        (ii) MOLECULE TYPE: cDNA
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
282
284 GTCTTTCTGC TCCCCACCCG CGGCCTGGAT GAAAAAAGC
                                                                            39
286 (2) INFORMATION FOR SEQ ID NO: 9:
288
        (i) SEQUENCE CHARACTERISTICS:
289
              (A) LENGTH: 66 base pairs
290
              (B) TYPE: nucleic acid
291
              (C) STRANDEDNESS: single
292
              (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: cDNA
294
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
296
298 TGCTCTAGAT TACTTGTCAT CGTCGTCCTT GTAGTCTGAT GTTTTAAAGT TAAGTTTTTT
                                                                           60
299 CCGGAG
                                                                           66
301 (2) INFORMATION FOR SEQ ID NO: 10:
         (i) SEQUENCE CHARACTERISTICS:
304
              (A) LENGTH: 5 amino acids
305
              (B) TYPE: amino acid
306
              (C) STRANDEDNESS: single
```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/961,201

DATE: 12/07/2001 TIME: 12:18:54

Input Set : N:\Crf3\RULE60\09961201.txt
Output Set: N:\CRF3\12072001\1961201.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]